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SEQUENCE LISTING

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WATAHIKI, Masanori

<120> RNA Polymerase

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<140> US 09/254,344

<141> 1999-09-03

<150> PCT/JP98/03037

<151> 1998-07-06

<150> JP 9/180883

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<151> 1998-06-04

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<170> PatentIn version 3.0

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Ala	Lys	His	Phe	Lys	Lys	Asn	Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	Val	170	
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 Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr Val Val Trp Ala
 785 790 795
 cac gag aag tac gga atc gaa tct ttt gca ctg att cac gac tcc ttc 2451
 His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp Ser Phe
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Met Ile Ala Arg Ile Asn Asp Trp Phe Glu Glu Val Lys Ala Lys Arg
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Gly Lys Arg Pro Thr Ala Phe Gln Phe Leu Gln Glu Ile Lys Pro Glu
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Ala Val Ala Tyr Ile Thr Ile Lys Thr Thr Leu Ala Cys Leu Thr Ser
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Ala Asp Asn Thr Thr Val Gln Ala Val Ala Ser Ala Ile Gly Arg Ala
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Ile Glu Asp Glu Ala Arg Phe Gly Arg Ile Arg Asp Leu Glu Ala Lys
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His Phe Lys Lys Asn Val Glu Glu Gln Leu Asn Lys Arg Val Gly His
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Val Tyr Lys Lys Ala Phe Met Gln Val Val Glu Ala Asp Met Leu Ser
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Lys Gly Leu Leu Gly Gly Glu Ala Trp Ser Ser Trp His Lys Glu Asp
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Ser Ile His Val Gly Val Arg Cys Ile Glu Met Leu Ile Glu Ser Thr
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Ser Glu Thr Ile Glu Leu Ala Pro Glu Tyr Ala Glu Ala Ile Ala Thr
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Val Pro Pro Lys Pro Trp Thr Gly Ile Thr Gly Gly Gly Tyr Trp Ala
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Met Asn Pro Glu Ala	Leu Thr Ala Trp Lys Arg	Ala Ala Ala Val				
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Tyr Arg Lys Asp Lys	Ala Arg Lys Ser Arg Arg	Ile Ser Leu Glu Phe				
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Met Leu Glu Gln Ala	Asn Lys Phe Ala Asn His	Lys Ala Ile Trp Phe				
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Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro Asn Gln
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Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser Val Thr
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Ala Arg Phe Arg Lys Met Phe Glu Arg Gln Leu Lys Ala Gly Glu Val
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705 710 715 720
 Leu Asn Leu Met Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn
 725 730 735
 Thr Asn Lys Asp Ser Glu Ile Asp Ala His Lys Gln Glu Ser Gly Ile
 740 745 750
 Ala Pro Asn Phe Val His Ser Gln Asp Gly Ser His Leu Arg Lys Thr
 755 760 765
 Val Val Trp Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile
 770 775 780
 His Asp Ser Phe Gly Thr Ile Pro Ala Asn Leu Phe Lys Ala Val Arg
 785 790 795 800
 Glu Thr Met Val Asp Thr Tyr Glu Ser Cys Asp Val Leu Ala Asp Phe
 805 810 815
 Tyr Asp Gln Phe Ala Asp Gln Leu His Glu Ser Gln Leu Asp Lys Met
 820 825 830
 Pro Ala Leu Pro Ala Lys Gly Asn Leu Asn Leu Arg Asp Ile Leu Glu
 835 840 845
 Ser Asp Phe Ala Phe Ala
 850

<210> 4
 <211> 852
 <212> PRT
 <213> Bacteriophage T3

<400> 4
 Met Asn Ile Ile Glu Asn Ile Glu Lys Asn Asp Phe Ser Glu Ile Glu
 1 5 10 15
 Leu Ala Ala Ile Pro Phe Asn Thr Leu Ala Asp His Tyr Gly Ser Ala
 20 25 30
 Leu Ala Lys Glu Gln Leu Ala Leu Glu His Glu Ser Tyr Glu Leu Gly
 35 40 45
 Glu Arg Arg Phe Leu Lys Met Leu Glu Arg Gln Ala Lys Ala Gly Glu
 50 55 60
 Ile Ala Asp Asn Ala Ala Ala Lys Pro Leu Leu Ala Thr Lys Leu Thr
 65 70 75 80
 Thr Arg Ile Val Glu Trp Leu Glu Glu Tyr Ala Ser Lys Lys Gly Arg
 85 90 95
 Lys Pro Ser Ala Tyr Ala Pro Leu Gln Leu Leu Lys Pro Glu Ala Ser
 100 105 110

Ala	Phe	Ile	Thr	Leu	Lys	Val	Ile	Leu	Ala	Ser	Leu	Thr	Ser	Thr	Asn	115	120	125
Met	Thr	Thr	Ile	Gln	Ala	Met	Leu	Gly	Lys	Ala	Ile	Glu	Asp	Glu	Ala	130	135	140
Arg	Phe	Gly	Arg	Ile	Arg	Asp	Leu	Glu	Ala	Lys	His	Phe	Lys	Lys	His	145	150	155
Val	Glu	Glu	Gln	Leu	Asn	Lys	Arg	His	Gly	Gln	Val	Tyr	Lys	Lys	Ala	165	170	175
Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Ile	Gly	Arg	Gly	Leu	Leu	Gly	180	185	190
Gly	Glu	Ala	Trp	Ser	Ser	Trp	Asp	Lys	Glu	Thr	Thr	Met	His	Val	Gly	195	200	205
Ile	Arg	Met	Leu	Ile	Glu	Ser	Thr	Gly	Leu	Val	Glu	Leu	Gln	Arg	His	210	215	220
Asn	Ala	Gly	Asn	Ala	Gly	Ser	Asp	His	Glu	Ala	Leu	Gln	Leu	Ala	Gln	225	230	235
Glu	Tyr	Val	Asp	Val	Leu	Ala	Lys	Ala	Gly	Ala	Leu	Ala	Gly	Ile	Ser	245	250	255
Pro	Met	Phe	Gln	Pro	Cys	Val	Val	Pro	Pro	Lys	Pro	Trp	Val	Ala	Ile	260	265	270
Thr	Gly	Gly	Gly	Tyr	Trp	Ala	Asn	Gly	Leu	Ala	Leu	Val	Arg	Thr	His	275	280	285
Ser	Lys	Lys	Gly	Leu	Met	Arg	Tyr	Glu	Asp	Val	Tyr	Met	Pro	Glu	Val	290	295	300
Tyr	Lys	Ala	Val	Asn	Leu	Ala	Gln	Asn	Thr	Ala	Trp	Lys	Ile	Asn	Lys	305	310	315
Lys	Val	Leu	Ala	Val	Val	Asn	Glu	Ile	Val	Asn	Trp	Lys	Asn	Cys	Pro	325	330	335
Val	Ala	Asp	Ile	Pro	Ser	Leu	Glu	Arg	Gln	Glu	Leu	Pro	Pro	Lys	Pro	340	345	350
Asp	Asp	Ile	Asp	Thr	Asn	Glu	Ala	Ala	Leu	Lys	Glu	Trp	Lys	Lys	Ala	355	360	365
Ala	Ala	Gly	Ile	Tyr	Arg	Leu	Asp	Lys	Ala	Arg	Val	Ser	Arg	Arg	Ile	370	375	380
Ser	Leu	Glu	Phe	Met	Leu	Glu	Gln	Ala	Asn	Lys	Phe	Ala	Ser	Lys	Lys	385	390	395
Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	Trp	Arg	Gly	Arg	Val	Tyr	Ala	405	410	415

Val Pro Met Phe Gly Asn Asp Met Thr Lys Gly Leu Leu Thr Leu Ala
 420 425 430
 Lys Gly Lys Pro Ile Gly Glu Glu Gly Phe Tyr Trp Leu Lys Ile His
 435 440 445
 Gly Ala Asn Cys Ala Gly Val Asp Lys Val Pro Phe Pro Glu Arg Ile
 450 455 460
 Ala Phe Ile Glu Lys His Val Asp Asp Ile Leu Ala Cys Ala Lys Asp
 465 470 475 480
 Pro Ile Asn Asn Thr Trp Trp Ala Glu Gln Asp Ser Pro Phe Ala Phe
 485 490 495
 Cys Phe Glu Tyr Ala Gly Val Thr His His Gly Leu Ser Tyr Asn Cys
 500 505 510
 Ser Leu Pro Leu Ala Phe Asp Gly Ser Cys Ser Gly Ile Gln His Phe
 515 520 525
 Ser Ala Met Leu Arg Asp Glu Val Gly Gly Arg Ala Val Asn Leu Leu
 530 535 540
 Pro Ser Glu Thr Val Gln Asp Ile Tyr Gly Ile Val Ala Gln Lys Val
 545 550 555 560
 Asn Glu Ile Leu Lys Gln Asn Gly Thr Pro Asn Glu Met Ile Thr Val
 565 570 575
 Thr Asp Lys Asp Thr Gly Glu Ile Ser Glu Lys Leu Lys Leu Gly Thr
 580 585 590
 Ser Thr Leu Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val
 595 600 605
 Thr Lys Arg Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly
 610 615 620
 Phe Arg Gln Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser
 625 630 635 640
 Gly Lys Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 645 650 655
 Ile Trp Asp Ala Val Ser Val Thr Val Val Ala Ala Val Glu Ala Met
 660 665 670
 Asn Trp Leu Lys Ser Ala Ala Lys Leu Leu Ala Ala Glu Val Lys Asp
 675 680 685
 Lys Lys Thr Lys Glu Ile Leu Arg His Arg Cys Ala Val His Trp Thr
 690 695 700
 Thr Pro Asp Gly Phe Pro Val Trp Gln Glu Pro Leu Gln Lys Arg Leu
 705 710 715 720

Asp Met Ile Phe Leu Gly Gln Phe Arg Leu Gln Pro Thr Ile Asn Thr
 725 730 735
 Leu Lys Asp Ser Gly Ile Asp Ala His Lys Gln Glu Ser Gly Ile Ala
 740 745 750
 Pro Asn Phe Val His Ser Gln Asp Gly Ser Arg Leu Met Thr Val Val
 755 760 765
 Tyr Ala His Glu Lys Tyr Gly Ile Glu Ser Phe Ala Leu Ile His Asp
 770 775 780
 Ser Phe Gly Thr Ile Pro Gly Lys Leu Phe Lys Ala Val Arg Glu Thr
 785 790 795 800
 Met Val Ile Thr Tyr Glu Asn Asn Asp Val Leu Ala Asp Phe Tyr Ser
 805 810 815
 Gln Phe Ala Asp Gln Leu His Glu Thr Gln Leu Asp Lys Met Pro Pro
 820 825 830
 Leu Pro Lys Lys Gly Asn Leu Asn Leu Gln Asp Ile Leu Lys Ser Asp
 835 840 845
 Phe Ala Phe Ala
 850

<210> 5
 <211> 876
 <212> PRT
 <213> Bacteriophage K11

<400> 5
 Met Asn Ala Leu Asn Ile Gly Arg Asn Asp Phe Ser Glu Ile Glu Leu
 1 5 10 15
 Ala Ala Ile Pro Tyr Asn Ile Leu Ser Glu His Tyr Gly Asp Gln Ala
 20 25 30
 Ala Arg Glu Gln Leu Ala Leu Glu His Glu Ala Tyr Glu Leu Gly Arg
 35 40 45
 Gln Arg Phe Leu Lys Met Leu Glu Arg Gln Val Lys Ala Gly Glu Phe
 50 55 60
 Ala Asp Asn Ala Ala Ala Lys Pro Leu Val Leu Thr Gln Leu Thr Lys
 65 70 75 80
 Arg Ile Asp Asp Trp Lys Glu Glu Gln Ala Asn Ala Arg Gly Lys Lys
 85 90 95
 Pro Arg Ala Tyr Tyr Pro Ile Lys His Gly Val Ala Ser Glu Leu Ala
 100 105 110
 Val Ser Met Gly Ala Glu Val Leu Lys Glu Lys Arg Gly Val Ser Ser
 115 120 125

Glu	Ala	Ile	Ala	Leu	Leu	Thr	Ile	Lys	Val	Val	Leu	Gly	Asn	Ala	His	130	135	140
Arg	Pro	Leu	Lys	Gly	His	Asn	Pro	Ala	Gln	Leu	Gly	Lys	Ala	Leu	Glu	145	150	155
Asp	Glu	Ala	Arg	Phe	Gly	Arg	Ile	Arg	Glu	Gln	Glu	Ala	Ala	Tyr	Phe	165	170	175
Lys	Lys	Asn	Val	Ala	Asp	Gln	Leu	Asp	Lys	Arg	Val	Gly	His	Val	Tyr	180	185	190
Lys	Lys	Ala	Phe	Met	Gln	Val	Val	Glu	Ala	Asp	Met	Ile	Ser	Lys	Gly	195	200	205
Met	Leu	Gly	Gly	Asp	Asn	Trp	Ala	Ser	Trp	Lys	Thr	Asp	Glu	Gln	Met	210	215	220
His	Val	Gly	Thr	Lys	Leu	Leu	Ile	Glu	Gly	Thr	Gly	Leu	Val	Glu	Met	225	230	235
Thr	Lys	Asn	Lys	Met	Ala	Asp	Gly	Ser	Asp	Asp	Val	Thr	Ser	Met	Gln	245	250	255
Met	Val	Gln	Leu	Ala	Pro	Ala	Phe	Val	Glu	Leu	Leu	Ser	Lys	Arg	Ala	260	265	270
Gly	Ala	Leu	Ala	Gly	Ile	Ser	Pro	Met	His	Gln	Pro	Cys	Val	Val	Pro	275	280	285
Pro	Lys	Pro	Trp	Val	Glu	Thr	Val	Gly	Gly	Gly	Tyr	Trp	Ser	Val	Gly	290	295	300
Leu	Ala	Leu	Val	Arg	Thr	His	Ser	Lys	Lys	Ala	Leu	Arg	Arg	Tyr	Ala	305	310	315
Asp	Val	His	Met	Pro	Glu	Val	Tyr	Lys	Ala	Val	Asn	Leu	Ala	Gln	Asn	325	330	335
Thr	Pro	Trp	Lys	Val	Asn	Lys	Lys	Val	Leu	Ala	Val	Val	Asn	Glu	Ile	340	345	350
Val	Asn	Trp	Lys	His	Cys	Pro	Val	Gly	Asp	Val	Pro	Ala	Ile	Glu	Arg	355	360	365
Glu	Glu	Leu	Pro	Pro	Arg	Pro	Asp	Asp	Ile	Asp	Thr	Asn	Glu	Val	Ala	370	375	380
Arg	Lys	Ala	Trp	Arg	Lys	Glu	Ala	Ala	Ala	Val	Tyr	Arg	Lys	Asp	Lys	385	390	395
Ala	Arg	Gln	Ser	Arg	Arg	Cys	Arg	Cys	Glu	Phe	Met	Val	Ala	Gln	Ala	405	410	415
Asn	Lys	Phe	Ala	Asn	His	Lys	Ala	Ile	Trp	Phe	Pro	Tyr	Asn	Met	Asp	420	425	430

Trp	Arg	Gly	Arg	Val	Tyr	Ala	Val	Ser	Met	Phe	Gly	Asn	Asp	Met	Thr	435	440	445
Lys	Gly	Ser	Leu	Thr	Leu	Ala	Lys	Gly	Lys	Pro	Ile	Gly	Leu	Asp	Gly	450	455	460
Phe	Tyr	Trp	Leu	Lys	Ile	His	Gly	Ala	Asn	Cys	Ala	Gly	Val	Asp	Lys	465	470	475
Val	Pro	Phe	Pro	Glu	Arg	Ile	Lys	Phe	Ile	Glu	Glu	Asn	Glu	Gly	Asn	485	490	495
Ile	Leu	Ala	Ser	Ala	Ala	Asp	Pro	Leu	Asn	Thr	Trp	Trp	Thr	Gln	Gln	500	505	510
Asp	Ser	Pro	Phe	Ala	Phe	Cys	Phe	Glu	Tyr	Ala	Gly	Val	Lys	His	His	515	520	525
Gly	Leu	Asn	Ser	Tyr	Asn	Cys	Ser	Leu	Pro	Leu	Ala	Phe	Asp	Gly	Ser	530	535	540
Cys	Ser	Gly	Ile	Gln	His	Phe	Ser	Ala	Met	Leu	Arg	Asp	Glu	Val	Gly	545	550	555
Gly	Arg	Ala	Val	Asn	Leu	Leu	Pro	Ser	Asp	Thr	Val	Asp	Ile	Tyr	Lys	565	570	575
Ile	Val	Ala	Asp	Lys	Val	Asn	Glu	Val	Leu	His	Gln	Asn	Gly	Ser	Gln	580	585	590
Thr	Val	Val	Glu	Gln	Ile	Ala	Asp	Lys	Glu	Thr	Gly	Glu	Phe	His	Glu	595	600	605
Lys	Val	Thr	Leu	Gly	Glu	Ser	Val	Leu	Ala	Ala	Gly	Gln	Trp	Leu	Gln	610	615	620
Tyr	Gly	Val	Thr	Arg	Lys	Val	Thr	Lys	Arg	Ser	Val	Met	Thr	Leu	Ala	625	630	635
Tyr	Gly	Ser	Lys	Glu	Ser	Leu	Val	Arg	Gln	Gln	Val	Leu	Glu	Asp	Thr	645	650	655
Ile	Gln	Pro	Ala	Ile	Asp	Asn	Gly	Glu	Phe	Thr	His	Gln	Pro	Asn	Gln	660	665	670
Ala	Ala	Gly	Tyr	Met	Ala	Lys	Leu	Ile	Asp	Ala	Ser	Thr	Ser	Val	Thr	675	680	685
Val	Val	Ala	Ala	Val	Glu	Ala	Met	Asn	Trp	Leu	Lys	Ser	Ala	Ala	Lys	690	695	700
Leu	Leu	Ala	Ala	Glu	Val	Lys	Asp	Lys	Lys	Lys	Gly	Val	Ile	Leu	His	705	710	715
Arg	Cys	Ala	Val	His	Trp	Val	Thr	Pro	Asp	Gly	Phe	Pro	Val	Trp	Gln	725	730	735

Glu Gln Asn Gln Ala Arg Leu Lys Leu Val Phe Leu Gly Gln Ala Asn
 740 745 750
 Val Lys Met Thr Tyr Asn Thr Gly Lys Asp Ser Glu Ile Asp Ala His
 755 760 765
 Lys Gln Glu Ser Gly Ile Ala Pro Asn Phe Val His Ser Gln Asp Gly
 770 775 780
 Ser His Leu Arg Met Thr Val Val His Ala Asn Glu Val Tyr Gly Ile
 785 790 795 800
 Asp Ser Phe Ala Leu Ile His Asp Ser Phe Gly Thr Ile Pro Gly Asn
 805 810 815
 Leu Phe Lys Ala Val Arg Glu Thr Met Val Lys Thr Tyr Glu Asp Asn
 820 825 830
 Asp Val Ile Ala Asp Phe Tyr Asp Gln Phe Ala Asp Gln Leu His Glu
 835 840 845
 Ser Gln Leu Asp Lys Met Pro Ala Val Pro Ala Lys Gly Asp Leu Asn
 850 855 860
 Leu Arg Asp Ile Leu Glu Ser Asp Phe Ala Phe Ala
 865 870 875

<210> 6
 <211> 841
 <212> PRT
 <213> Bacteriophage SP6

<400> 6
 Met Gln Asp Leu His Ala Ile Gln Leu Gln Leu Glu Glu Glu Met Phe
 1 5 10 15
 Asn Gly Gly Ile Arg Arg Phe Glu Ala Asp Gln Gln Arg Gln Ile Ala
 20 25 30
 Ala Gly Ser Glu Ser Asp Thr Ala Trp Asn Arg Arg Leu Leu Ser Glu
 35 40 45
 Pro Met Ala Glu Gly Ile Gln Ala Tyr Lys Glu Glu Tyr Glu Gly Lys
 50 55 60
 Lys Gly Arg Ala Pro Arg Ala Leu Ala Phe Leu Gln Cys Val Glu Asn
 65 70 75 80
 Glu Val Ala Ala Tyr Ile Thr Met Lys Val Val Met Asp Met Leu Asn
 85 90 95
 Thr Asp Ala Thr Leu Gln Ser Val Ala Glu Arg Ile Glu Asp Gln Val
 100 105 110
 Arg Phe Ser Lys Leu Glu Gly His Ala Ala Lys Tyr Phe Glu Lys Val
 115 120 125

Lys	Lys	Ser	Leu	Lys	Ala	Ser	Arg	Thr	Lys	Ser	Tyr	Arg	His	Ala	His	130	135	140
Asn	Val	Ala	Val	Val	Ala	Glu	Lys	Ser	Val	Ala	Glu	Lys	Asp	Ala	Asp	145	150	155
Phe	Asp	Arg	Trp	Glu	Ala	Trp	Pro	Lys	Glu	Thr	Gln	Leu	Gln	Ile	Gly	165	170	175
Thr	Thr	Ile	Leu	Glu	Gly	Ser	Val	Phe	Tyr	Asn	Gly	Glu	Pro	Val	Phe	180	185	190
Met	Arg	Ala	Met	Arg	Thr	Tyr	Gly	Gly	Lys	Thr	Ile	Tyr	Tyr	Leu	Gln	195	200	205
Thr	Ser	Glu	Ser	Val	Gly	Gln	Trp	Ile	Ser	Ala	Phe	Lys	Glu	His	Val	210	215	220
Ala	Gln	Leu	Ser	Pro	Ala	Tyr	Ala	Pro	Cys	Val	Ile	Pro	Pro	Arg	Pro	225	230	235
Trp	Arg	Thr	Pro	Phe	Asn	Gly	Gly	Phe	His	Thr	Glu	Lys	Val	Ile	Arg	245	250	255
Leu	Val	Lys	Gly	Asn	Arg	Glu	His	Val	Arg	Lys	Leu	Thr	Gln	Lys	Gln	260	265	270
Met	Pro	Lys	Val	Tyr	Lys	Ala	Ile	Asn	Ala	Leu	Gln	Asn	Thr	Gln	Trp	275	280	285
Gln	Ile	Asn	Lys	Asp	Val	Leu	Ala	Val	Ile	Glu	Glu	Val	Ile	Arg	Leu	290	295	300
Asp	Leu	Gly	Tyr	Gly	Val	Pro	Ser	Phe	Lys	Pro	Leu	Ile	Asp	Lys	Glu	305	310	315
Asn	Lys	Pro	Ala	Asn	Pro	Val	Pro	Val	Glu	Leu	Arg	Gly	Arg	Glu	Leu	325	330	335
Lys	Glu	Met	Leu	Ser	Pro	Glu	Gln	Trp	Gln	Gln	Phe	Ile	Asn	Trp	Lys	340	345	350
Gly	Glu	Cys	Ala	Arg	Leu	Tyr	Thr	Ala	Glu	Thr	Lys	Arg	Gly	Ser	Lys	355	360	365
Ser	Ala	Ala	Val	Val	Arg	Met	Val	Gly	Gln	Ala	Arg	Lys	Tyr	Ser	Ala	370	375	380
Phe	Glu	Ser	Ile	Tyr	Phe	Val	Tyr	Ala	Met	Asp	Ser	Arg	Ser	Arg	Val	385	390	395
Tyr	Val	Gln	Ser	Ser	Thr	Leu	Ser	Asn	Asp	Leu	Gly	Lys	Ala	Leu	Leu	405	410	415
Arg	Phe	Thr	Glu	Gly	Arg	Pro	Val	Asn	Gly	Val	Glu	Ala	Leu	Lys	Trp	420	425	430

Phe Cys Ile Asn Gly Ala Asn Leu Trp Gly Trp Asp Lys Lys Thr Phe
 435 440 445
 Asp Val Arg Val Ser Asn Val Leu Asp Glu Glu Phe Gln Asp Met Cys
 450 455 460
 Arg Asp Ile Ala Ala Asp Pro Leu Thr Phe Thr Gln Trp Ala Lys Ala
 465 470 475 480
 Asp Ala Pro Tyr Ala Trp Cys Phe Glu Tyr Ala Gln Tyr Leu Asp Leu
 485 490 495
 Val Asp Glu Gly Arg Ala Asp Glu Phe Arg Thr His Leu Pro Val His
 500 505 510
 Gln Asp Gly Ser Cys Ser Gly Ile Gln His Tyr Ser Ala Met Leu Arg
 515 520 525
 Asp Glu Val Gly Ala Lys Ala Val Asn Leu Lys Pro Ser Asp Ala Pro
 530 535 540
 Gln Asp Ile Tyr Gly Ala Val Ala Gln Val Val Ile Asn Ala Leu Tyr
 545 550 555 560
 Met Asp Ala Asp Asp Ala Thr Thr Phe Thr Ser Gly Ser Val Thr Leu
 565 570 575
 Ser Gly Thr Glu Leu Arg Ala Met Ala Ser Ala Trp Asp Ser Ile Gly
 580 585 590
 Ile Thr Arg Ser Leu Thr Lys Lys Pro Val Met Thr Leu Pro Tyr Gly
 595 600 605
 Ser Thr Arg Leu Thr Cys Arg Glu Ser Val Ile Asp Tyr Ile Val Asp
 610 615 620
 Leu Glu Glu Lys Glu Ala Gln Lys Glu Gly Arg Thr Ala Asn Lys Val
 625 630 635 640
 His Pro Phe Glu Asp Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 645 650 655
 Tyr Asn Tyr Met Thr Ala Leu Ile Trp Pro Ser Ile Ser Glu Val Val
 660 665 670
 Lys Ala Pro Ile Val Ala Met Lys Met Ile Arg Gln Leu Ala Arg Phe
 675 680 685
 Ala Ala Lys Arg Asn Glu Gly Leu Met Tyr Thr Leu Pro Thr Gly Phe
 690 695 700
 Ile Leu Glu Gln Lys Thr Glu Met Leu Arg Val Arg Thr Cys Leu Met
 705 710 715 720
 Gly Asp Ile Lys Met Ser Leu Gln Val Glu Thr Asp Ile Val Asp Glu
 725 730 735

Ala Ala Met Met Gly Ala Ala Ala Pro Asn Phe Val His Gly His Asp
 740 745 750

Ala Ser His Leu Ile Leu Thr Val Cys Glu Leu Val Asp Lys Gly Val
 755 760 765

Thr Ser Ile Ala Val Ile His Asp Ser Phe Gly Thr His Ala Leu Thr
 770 775 780

Leu Arg Val Ala Leu Lys Gly Gln Met Val Ala Met Tyr Ile Asp Gly
 785 790 795 800

Asn Ala Leu Gln Lys Leu Leu Glu Glu His Glu Val Arg Trp Met Val
 805 810 815

Asp Thr Gly Ile Glu Val Pro Glu Gln Gly Glu Phe Asp Leu Asn Glu
 820 825 830

Ile Met Asp Ser Glu Tyr Val Phe Ala
 835 840

<210> 7
 <211> 78
 <212> PRT
 <213> Bacteriophage T7

<400> 7
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 8
 <211> 78
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(78)
 <223> Mutant T7 RNA polymerase F644Y.

<400> 8
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15

Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30
 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45
 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Thr Trp Glu Ser Val Ser
 50 55 60
 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 9
 <211> 78
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(78)
 <223> Mutant T7 RNA polymerase F646Y.

<400> 9
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15
 Tyr Gly Ser Lys Glu Phe Gly Tyr Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30
 Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Leu Met Phe Thr Gln Pro
 35 40 45
 Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60
 Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 10
 <211> 78
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(78)
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 10
 Tyr Gly Val Thr Arg Ser Val Thr Lys Arg Ser Val Met Thr Leu Ala
 1 5 10 15
 Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln Gln Val Leu Glu Asp Thr
 20 25 30

Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly Pro Met Tyr Thr Gln Pro
 35 40 45

Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu Ile Trp Glu Ser Val Ser
 50 55 60

Val Thr Val Val Ala Ala Val Glu Ala Met Asn Trp Leu Lys
 65 70 75

<210> 11
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<400> 11
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 12
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase F644Y.

<400> 12
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Tyr Gly Phe Arg Gln
 20 25 30

Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45

Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60

Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 13
 <211> 73
 <212> PRT
 <213> Bacteriophage T7

<220>
 <221> PEPTIDE
 <222> (1)..(73)
 <223> Mutant T7 RNA polymerase L665P/F667Y.

<400> 13
 Ala Gly Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45
 Pro Met Tyr Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60
 Ile Trp Glu Ser Val Ser Val Thr Val
 65 70

<210> 14
 <211> 73
 <212> PRT
 <213> Bacteriophage T3

<400> 14
 Ala Gln Gln Trp Leu Ala Tyr Gly Val Thr Arg Ser Val Thr Lys Arg
 1 5 10 15
 Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Phe Gly Phe Arg Gln
 20 25 30
 Gln Val Leu Asp Asp Thr Ile Gln Pro Ala Ile Asp Ser Gly Lys Gly
 35 40 45
 Leu Met Phe Thr Gln Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60
 Ile Trp Asp Ala Val Ser Val Thr Val
 65 70

<210> 15
 <211> 73
 <212> PRT
 <213> Bacteriophage K11

<400> 15
 Ala Ala Gln Trp Leu Gln Tyr Gly Val Thr Arg Lys Val Thr Lys Arg
 1 5 10 15

Ser Val Met Thr Leu Ala Tyr Gly Ser Lys Glu Ser Leu Val Arg Gln
 20 25 30
 Gln Val Leu Glu Asp Thr Ile Gln Pro Ala Ile Asp Asn Gly Glu Gly
 35 40 45
 Leu Met Phe Thr His Pro Asn Gln Ala Ala Gly Tyr Met Ala Lys Leu
 50 55 60
 Ile Trp Asp Ala Val Thr Val Thr Val
 65 70

<210> 16
 <211> 75
 <212> PRT <
 213> Bacteriophage SP6

<400> 16
 Ala Ser Ala Trp Asp Ser Ile Gly Ile Thr Arg Ser Leu Thr Lys Lys
 1 5 10 15
 Pro Val Met Thr Leu Pro Tyr Gly Ser Thr Arg Leu Thr Cys Arg Glu
 20 25 30
 Ser Val Ile Asp Tyr Ile Val Asp Leu Glu Glu Lys Glu Ala Gln Lys
 35 40 45
 Ala Val Ala Glu Gly Arg Thr Ala Asn Lys Val His Pro Phe Glu Asp
 50 55 60
 Asp Arg Gln Asp Tyr Leu Thr Pro Gly Ala Ala
 65 70 75

<210> 17
 <211> 31
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(31)
 <223> Mutant T7 RNA polymerase wild type.

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> Nucleotide 25 is "n" wherein "n" = any nucleotide.

<400> 17
 gggagggggg ggggggggcc ccccnngggcg t

31

<210> 18
 <211> 32
 <212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(32)

<223> Mutant T7 RNA polymerase wild type.

<220>

<221> misc_feature

<222> (1)..(32)

<223> Nucleotides 6-8, 18, 25-30 are "n" wherein "n" = any nucleotide.

<400> 18

gcgtcnnnaa aacgcacntt ttctntcgtn gg

32

<210> 19

<211> 19

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(19)

<223> Mutant T7 RNA polymerase F644Y.

<400> 19

cgaggggggg ccggtaccc

19

<210> 20

<211> 25

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(25)

<223> Mutant T7 RNA polymerase F644Y.

<220>

<221> misc_feature

<222> (6)..(6)

<223> Nucleotide 6 is "n" wherein "n" = any nucleotide.

<400> 20

cccctntttg ttcctttagt gaggt

25

<210> 21

<211> 18

<212> DNA

<213> Bacteriophage T7

<220>

<221> misc_feature

<222> (1)..(18)
 <223> Mutant T7 RNA polymerase F667Y.

<400> 21
 gagggggggcc ggtaacgc

18

<210> 22
 <211> 22
 <212> DNA
 <213> Bacteriophage T7

<220>
 <221> misc_feature
 <222> (1)..(22)
 <223> Mutant T7 RNA polymerase F667Y.

<400> 22
 acgccttttg ttcccttttag tg

22

<210> 23
 <211> 569
 <212> DNA
 <213> Bacteriophage T7
 <220>
 <221> misc_feature
 <222> (1)..(569)
 <223> Mutant T7 RNA polymerase F644Y/L665P/F667Y.

<220>
 <221> misc_feature
 <222> (1)..(472)
 <223> Nucleotides 1-14, 17-18, 21, 26, 29, 34, 38, 40, 50-51, 53, 58, 7
 5-76, 85, 110, 117, 132, 142, 150, 157, 399, 440 and 472 are "n"
 wherein "n" = any nucleotide

<400> 23
 nnnnnnnnnn nnnnggnngt nggttncgna tccnaaangn aacaggggggn nantgtgnaa 60
 acatgaatat ttttnntaag ctttnattcc agggcaagac attttaaccn aaattgncaa 120
 attatatcac tnattagaca gnaaaatctn acccagntaa gacttctgga ggtttggtac 180
 agtagtttgt cttggatgct tcatgtatgc agtcacttat agtcagtatt gcacttggca 240
 cacttcagct taaaccaaca ggataggaaa aatagggagc aacatggagt ggcacacctg 300
 tatttctaca gtctgtaga tgaagtctct atatgtgcaa catcctggga cagagcatat 360
 ttgggaagaa acagtttgcc attgaatccc gtgtcatana atatccagca cagatgggtg 420
 tgttgatggt tagcaataan cacactctct ctttctgatg tgcattgtat antcaggtgg 480
 atacaaaaag acatcgcttg gccacatgc aaggccaaaa agcagacatc agaaagagag 540
 cagtcatgtg ggggaattgg tccgactgc 569